

IN THE CLAIMS:

Claims 30, 31, 35, 38, and 39 have been amended. Claims 46-49 have been cancelled. New claims 50-55 have been added. Claims 30-45 and 50-55 are pending in the present application. The following is the status of the claims of the above-captioned application, as amended.

1-29 (Cancelled)

30. (Currently Amended) An isolated nucleic acid sequence encoding a polypeptide having carboxypeptidase activity, selected from the group consisting of:

(a) a nucleic acid sequence encoding a polypeptide having an amino acid sequence which has at least ~~70%~~ 80% identity with amino acids 19 to 555 of SEQ ID NO. 2;

(b) a nucleic acid sequence having at least ~~70%~~ 80% homology with nucleotides 55 to 1662 of SEQ ID NO. 1; and

(c) a nucleic acid sequence which hybridizes under medium stringency conditions with (i) nucleotides 55 to 1662 of SEQ ID NO. 1, (ii) ~~a subsequence of (i) of at least 100 nucleotides,~~ or (iii) ~~a its~~ its complementary strand ~~of (i) or (ii),~~ wherein medium stringency conditions are defined as prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 mg/ml sheared and denatured salmon sperm DNA, and 35% formamide;

~~(d) a subsequence of (a), (b), or (c), wherein the subsequence encodes a polypeptide fragment which has carboxypeptidase activity; and~~

~~(e) a nucleic acid sequence encoding a polypeptide having carboxypeptidase activity with (i) an optimal activity in the range of about pH 4.0 to about pH 5.0 at 25°C; (ii) an optimal activity in the range of about 55°C to about 60°C at pH 4; (iii) a residual activity of at least about 65.5% after 30 minutes at pH 4.0 and 60°C; and (iv) an ability to hydrolyze X from N-CBZ-Ala-X wherein N-CBZ is N-carbobenzoxy and X is any amino acid.~~

31. (Currently Amended) The nucleic acid sequence of claim 30, which encodes a polypeptide having an amino acid sequence which has at least ~~70%~~ 80% identity with amino acids 19 to 555 of SEQ ID NO. 2.

32. (Previously Presented) The nucleic acid sequence of claim 30, which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO. 2.

33. (Previously Presented) The nucleic acid sequence of claim 30, which encodes a polypeptide consisting of the amino acid sequence of SEQ ID NO. 2, or a fragment thereof which has carboxypeptidase activity.

34. (Previously Presented) The nucleic acid sequence of claim 33, which encodes a polypeptide consisting of the amino acid sequence of SEQ ID NO. 2.

35. (Currently Amended) The nucleic acid sequence of claim ~~34~~ 33, which encodes a polypeptide consisting of amino acids 19 to 555 of SEQ ID NO. 2.

36. (Currently Amended) The nucleic acid sequence of claim 30, which has at least ~~70%~~ 80% homology with the nucleic acid sequence of SEQ ID NO. 1.

37. (Previously Presented) The nucleic acid sequence of claim 30, which has the nucleic acid sequence of SEQ ID NO. 1.

38. (Currently Amended) The nucleic acid sequence of claim 30, wherein the nucleic acid sequence hybridizes under medium stringency conditions with (i) nucleotides 55 to 1662 of SEQ ID NO. 1, (ii) ~~a subsequence of (i) of at least 100 nucleotides,~~ or (iii) ~~a~~ its complementary strand ~~of (i) or (ii),~~ wherein medium stringency conditions are defined as prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 mg/ml sheared and denatured salmon sperm DNA, and 35% formamide.

39. (Currently Amended) The nucleic acid sequence of claim 30, wherein the nucleic acid sequence hybridizes under high stringency conditions with (i) nucleotides 55 to 1662 of SEQ ID NO. 1, (ii) ~~a subsequence of (i) of at least 100 nucleotides,~~ or (iii) ~~a~~ its complementary strand ~~of (i) or (ii),~~ wherein ~~medium~~ high stringency conditions are defined as prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 mg/ml sheared and denatured salmon sperm DNA, and 50% formamide.

40. (Previously Presented) The nucleic acid sequence of claim 30, which encodes a polypeptide having carboxypeptidase activity with (i) an optimal activity in the range of about pH 4.0 to about pH 5.0 at 25°C; (ii) an optimal activity in the range of about 55°C to about 60°C at pH 4; (iii) a residual activity of at least about 65.5% after 30 minutes at pH 4.0 and 60°C; and (iv) an ability to hydrolyze X from N-CBZ-Ala-X wherein N-CBZ is N-carbobenzoxy and X is any amino acid.

41. (Previously Presented) The nucleic acid sequence of claim 30, which is contained in the plasmid pEJG12 which is contained in *E. coli*, NRRL B-21616.

42. (Previously Presented) A nucleic acid construct comprising the nucleic acid sequence of claim 30 operably linked to one or more control sequences which direct the production of the polypeptide in a suitable expression host.

43. (Previously Presented) A recombinant expression vector comprising the nucleic acid construct of claim 42.

44. (Previously Presented) A recombinant host cell comprising the nucleic acid construct of claim 42.

45. (Previously Presented) A method for producing a polypeptide having carboxypeptidase activity comprising (a) cultivating the host cell of claim 44 under conditions suitable for production of the polypeptide; and (b) recovering the polypeptide.

46. (Canceled).

47. (Canceled).

48. (Canceled).

49. (Canceled).

50. (New) The nucleic acid sequence of claim 31, which encodes a polypeptide having an amino acid sequence which has at least 85% identity with amino acids 19 to 555 of SEQ ID NO. 2.

51. (New) The nucleic acid sequence of claim 50, which encodes a polypeptide having an amino acid sequence which has at least 90% identity with amino acids 19 to 555 of SEQ ID NO. 2.

52. (New) The nucleic acid sequence of claim 51, which encodes a polypeptide having an amino acid sequence which has at least 95% identity with amino acids 19 to 555 of SEQ ID NO. 2.

53. (New) The nucleic acid sequence of claim 36, which has at least 85% homology with the nucleic acid sequence of SEQ ID NO. 1.

54. (New) The nucleic acid sequence of claim 53, which has at least 90% homology with the nucleic acid sequence of SEQ ID NO. 1.

55. (New) The nucleic acid sequence of claim 54, which has at least 95% homology with the nucleic acid sequence of SEQ ID NO. 1.